

IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/754,014A

DATE: 08/23/2004 TIME: 16:08:38

Input Set : A:\09-754,014.txt

Output Set: N:\CRF4\08232004\1754014A.raw

```
3 <110> APPLICANT: Valentis, Inc.
       Nordstrom, Jeff
         Freimark, Bruce
         Deshpande, Deepa
 8 <120> TITLE OF INVENTION: Gene Expression and Delivery Systems and Uses
10 <130> FILE REFERENCE: 213-0063US
12 <140> CURRENT APPLICATION NUMBER: US 09/754,014A
13 <141> CURRENT FILING DATE: 2001-01-03
15 <150> PRIOR APPLICATION NUMBER: US 08/948,958
16 <151> PRIOR FILING DATE: 1997-10-10
18 <150> PRIOR APPLICATION NUMBER: US 60/028,687
19 <151> PRIOR FILING DATE: 1996-10-10
21 <160> NUMBER OF SEQ ID NOS: 19
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 328
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
32 Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
                                       10
36 Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
37
40 Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
41
                               40
44 Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln
48 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
                       70
52 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
56 Leu Ser His Ser Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
              100
                                   105
60 Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
64 Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
       130
                           135
68 Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
69 145
72 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
                   165
                                       170
76 Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
                                   185
```

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```
80 Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
           195
84 Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
                                                220
85
       210
                           215
88 Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
                       230
                                            235
92 Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
                                        250
                   245
  Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
                                    265
100 Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
                                                     285
            275
                                280
104 Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
                            295
108 Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
109 305
                        310
                                             315
                                                                 320
112 Glu Trp Ala Ser Val Pro Cys Ser
113
116 <210> SEO ID NO: 2
117 <211> LENGTH: 987
118 <212> TYPE: DNA
119 <213> ORGANISM: homo sapiens
121 <400> SEQUENCE: 2
122 atgtgtcacc agcagttggt catctcttgg ttttccctgg tttttctggc atctcccctc
                                                                            60
124 gtggccatat gggaactgaa gaaagatgtt tatgtcgtag aattggattg gtatccggat
                                                                           120
126 gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg
                                                                           180
128 accttggacc agagcagtga ggtcttaggc tetggcaaaa ceetgaccat ccaagtcaaa
                                                                           240
130 gagtttggag atgctggcca gtacacctgt cacaaaggag gcgaggttct aagccattcg
                                                                           300
132 ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatttt aaaggaccag
                                                                           360
                                                                           420
134 aaagaaccca aaaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc
136 acctqctqqt qqctqacqac aatcaqtact qatttqacat tcaqtqtcaa aagcagcaga
                                                                           480
138 ggctcttctg acccccaagg ggtgacgtgc ggagctgcta cactctctgc agagagagtc
                                                                           540
                                                                           600
140 agaggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgccca
142 getgetgagg agagtetgee cattgaggte atggtggatg cegtteacaa geteaagtat
                                                                           660
144 gaaaactaca ccagcagett etteateagg gacateatea aacetgaeee aeeeaagaae
                                                                           720
146 ttgcagctga agccattaaa gaattctcgg caggtggagg tcagctggga gtaccctgac
                                                                           780
                                                                           840
148 acctggagta ctccacattc ctacttctcc ctgacattct gcgttcaggt ccagggcaag
                                                                           900
150 agcaagagag aaaagaaaga tagagtette aeggacaaga eeteageeae ggteatetge
152 cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttggagc
                                                                           960
                                                                           987
154 gaatgggcat ctgtgccctg cagttag
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 987
159 <212> TYPE: DNA
160 <213> ORGANISM: artificial sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: codon optimized Human IL-12 p40
165 <400> SEQUENCE: 3
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                                                                            60
168 gtqqccatct qqqaqctqaa qaaggacgtg tacgtggtgg agctggactg gtaccccgac
                                                                           120
```

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```
170 gcccccggcg agatggtggt gctgacctgc gacacccccg aggaggacgg catcacctgg
                                                                      180
                                                                      240
172 accetggace agageagega ggtgetggge ageggeaaga ceetgaceat ceaggtgaag
                                                                      300
174 gaqttcqqcq acqccqqcca qtacacctqc cacaagggcg gcgaggtgct gagccacagc
176 ctgctgctgc tgcacaagaa ggaggacggc atctggagca ccgacatcct gaaggaccag
                                                                      360
178 aaggageeca agaacaagae etteetgege tgegaggeea agaactacag eggeegette
                                                                      420
480
182 qqcaqcaqcq acccccaggq cgtgacctgc ggcgccgcca ccctgagcgc cgagcgcgtg
                                                                      540
                                                                      600
184 egeggegaca acaaggagta egagtacage gtggagtgee aggaggacag egeetgeece
                                                                      660
186 geogeogagg agageotgee categaggtg atggtggacg cegtecacaa getgaagtac
188 gagaactaca ccagcagctt cttcatccgc gacatcatca agcccgaccc ccccaagaac
                                                                      720
190 ctgcagctga agcccctgaa gaacagccgc caggtggagg tgagctggga gtaccccgac
                                                                      780
                                                                      840
192 acctggagca cccccacag ctacttcagc ctgaccttct gcgtgcaggt gcagggcaag
                                                                      900
194 agcaagegeg agaagaagga cegegtgtte acegacaaga ceagegeeac egtgatetge
196 cgcaagaacg ccagcatcag cgtgcgccc caggaccgct actacagcag cagctggagc
                                                                      960
198 gagtgggcca gcgtgccctg cagctag
                                                                      987
201 <210> SEQ ID NO: 4
202 <211> LENGTH: 987
203 <212> TYPE: DNA
204 <213> ORGANISM: artificial sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: codon optimized human IL-12 p40
209 <400> SEQUENCE: 4
210 atgtgccacc agcagetggt gateagetgg ttetecetgg tgtttetgge eageeceete
                                                                       60
212 qtqqccatct qqqaqctgaa gaaaqacgtg tacgtggtcg agctggactg gtaccccgac
                                                                      120
214 geoceeggeg agatggtggt cetgacetge gacaceceeg aggaagaegg catcacetgg
                                                                      180
216 accotggacc agagcagtga ggtgctgggc tccggcaaga ccctgaccat ccaggtgaag
                                                                      240
                                                                      300
218 gagtteggeg aegeeggeea gtacacetge cacaagggag gegaggtget gagecactee
220 etectgetge tecacaaaaa ggaggaegge atetggagea eegacateet gaaggaeeag
                                                                      360
                                                                      420
222 aaggagccca agaacaagac etteetgege tgegaggeea agaactacag eggeegette
                                                                      480
226 ggctccagcg accccaggg cgtgacctgc ggcgctgcca ccctgagcgc cgagcgcgtg
                                                                      540
228 cgcggcgaca acaaggagta cgagtacagc gtggagtgcc aggaagactc cgcctgcccc
                                                                      600
230 gccgctgagg agagcctgcc catcgaggtg atggtggacg ccgttcacaa gctgaagtac
                                                                      660
232 gagaactaca ccagcagett etteateege gacateatea ageetgaeee acceaagaac
                                                                      720
234 ctccagctga agcccctcaa gaactcccgc caggtggagg tgagctggga gtaccccgac
                                                                      780
236 acctqgagca cgccccactc ctacttctcc ctgaccttct gcgtgcaggt ccagggcaag
                                                                      840
238 agcaagegeg agaagaaaga cegggtgtte acegacaaga ceagegeeac egteatetge
                                                                      900
240 cgcaagaacg ccagcatcag cgtgcgcgcc caggaccgct actatagctc ctcttggagc
                                                                      960
                                                                      987
242 gagtgggcca gcgtgccctg ctcctag
245 <210> SEQ ID NO: 5
246 <211> LENGTH: 219
247 <212> TYPE: PRT
248 <213> ORGANISM: homo sapiens
250 <400> SEQUENCE: 5
252 Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
253 1
                                      10
256 Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
260 Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
```

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Input Set : A:\09-754,014.txt

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261		35					40					45				
264	Ser As	n Met	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Pro	Cys	
265	50)				55					60				_	
268	Thr Se	er Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser	
269					70					75					80	
272	Thr Va	ıl Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Thr	Lys	Asn	Glu	Ser	Cys	
273				85					90					95		
276	Leu As	n Ser	Arg	Glu	Thr	Ser	Phe	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	
277			100					105					110			
280	Ser Ar	g Lys	Thr	Ser	Phe	Met	Met	Ala	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	
281		115					120					125				
	Glu As		Lys	Met	Tyr		Val	Glu	Phe	Lys	Thr	Met	Asn	Ala	Lys	
285	13					135					140					
	Leu Le	u Met	Asp	Pro		Arg	Gln	Ile	Phe		Asp	Gln	Asn	Met		
	145			_	150		_			155					160	
	Ala Va	ıl Ile	Asp		Leu	Met	Gln	Ala		Asn	Phe	Asn	Ser		Thr	
293	_ _	,		165					170					175		
	Val Pr	o GIn		Ser	Ser	Leu	Glu			Asp	Phe	Tyr		Thr	Lys	
297	- 1 -	-	180		_	_		185		_		_	190		•	
	Ile Ly		Cys	11e	Leu	Leu		Ala	Phe	Arg	Ile		Ala	Val	Thr	
301	T] - 7-	195	T7 1	ml	0	m	200	7	7 7 - '	0		205				
304	Ile As		Val	THE	ser	215	Leu	ASII	Ala	ser						
	<210>		ח או			215										
	<211>														•	
				30												
	<212> TYPE: DNA <213> ORGANISM: homo sapiens															
	<400> SEQUENCE: 6															
														60		
	ttggcc															120
																180
														240		
															300	
324	gagacetett teataaetaa tgggagttge etggeeteea gaaagaeete ttttatgatg													360		
	gccctgtgcc ttagtagtat ttatgaagac ttgaagatgt accaggtgga gttcaagacc													420		
328	atgaat	gcaa	agctt	ctga	it go	gatco	taag	gago	gcaga	atct	ttct	agat	ca a	aaada	atgctg	480
330	gcagttattg atgagctgat gcaggccctg aatttcaaca gtgagactgt gccacaaaaa 54														540	
332	tcctcc	cttg	aagaa	accgg	ga tt	ttta	itaaa	act	aaaa	atca	agct	ctgo	at a	actto	cttcat	600
334	gctttc	agaa	ttcg	ggcag	ıt ga	ctat	tgad	: aga	igtga	acga	gcta	itcts	gaa t	gctt	cctaa	660
337	<210>	SEQ I	D NO	: 7									•			
338	<211>	LENGT	H: 66	50				•								
	<212>												*			
	<213> ORGANISM: artificial sequence															
		<220> FEATURE:														
	<223> OTHER INFORMATION: Codon optimized Human IL-12 p35															
	<400>															
	atgtgc															60
	ctggcc															120
350	agccag	aacc	tgctg	gcgg	ic cō	rtgag	caac	: atg	ctgo	aga	aggo	cgcg	ca ç	jacco	tggag	180

RAW SEQUENCE LISTING DATE: 08/23/2004 PATENT APPLICATION: US/09/754,014A TIME: 16:08:38

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```
352 ttctacccct gcaccagcga ggagatcgac cacgaggaca tcaccaagga caagaccagc
                                                                          240
354 acceptegage cetecetece ectegagete accaagaace aqaqetecet qaacaqeeqe
                                                                          300
356 gagaccaget teateaceaa eggeagetge etggeeagee geaagaccag etteatgatg
                                                                          360
358 gccctgtgcc tgagcagcat ctacgaggac ctgaagatgt accaggtgga gttcaagacc
                                                                          420
360 atgaacgcca agctgctgat ggaccccaag ctccagatct tcctggacca gaacatgctg
                                                                          480
362 geegtgateg aegagetgat geaggeeetg aactteaaea gegagaeegt geeeeagaag
                                                                          540
364 agcagectgg aggagecega ettetacaag accaagatea agetgtgeat eetgetgeae
                                                                          600
366 geetteegea teegegeegt gaccategae egegtgaeea getaeetgaa egeeaeetga
                                                                          660
369 <210> SEQ ID NO: 8
370 <211> LENGTH: 660
371 <212> TYPE: DNA
372 <213> ORGANISM: artificial sequence
374 <220> FEATURE:
375 <223> OTHER INFORMATION: codon optimized Human IL-12 p35
377 <400> SEQUENCE: 8
378 atgtgccccg cccgcagcct gctgctcgtg gccaccctgg tgctcctgga ccacctcagc
                                                                           60
380 etggecegea aceteceegt ggecaceeca gaceeeggea tgtteceatg cetgeaceae
                                                                          120
382 agccagaacc tgctggcggc cgtgagcaac atgctgcaga aggccgcgca gaccctggag
                                                                          180
384 ttctacccct gcaccagcga ggagatcgac cacgaggaca tcaccaagga caagaccagc
                                                                          240
386 accgtggagg cctgcctgcc cctcgagtta accaagaacg agagctgcct caacagccgc
                                                                          300
388 gagacetect teateaceaa eggeaettge etggeetece geaagaceag etteatgatg
                                                                          360
390 gecetgtgee tgageteeat etacgaggae etgaagatgt accaggtgga gtteaagace
                                                                          420
392 atgaacgeca ageteetgat ggaccecaag etecagatet teetggacca gaacatgetg
                                                                          480
394 gccgtgatcg acgagctgat gcaggccctg aacttcaaca gcgagaccgt gccccagaag
                                                                          540
396 agcagcetgg aggagecega ettetacaag accaagatea agetqtqcat cetqctqcae
                                                                          600
398 gccttccgca tccgggccgt gaccatcgac cgcgtgacca gctacctgaa cgccacqtqa
                                                                          660
401 <210> SEO ID NO: 9
402 <211> LENGTH: 58
403 <212> TYPE: DNA
404 <213> ORGANISM: artificial sequence
406 <220> FEATURE:
407 <223> OTHER INFORMATION: synthetic 5' UTR
409 <400> SEQUENCE: 9
410 aagettaete aacacaataa caaacttaet tacaatetta attaacaqqe caccatqq
413 <210> SEQ ID NO: 10
414 <211> LENGTH: 45
415 <212> TYPE: DNA
416 <213> ORGANISM: artificial sequence
418 <220> FEATURE:
419 <223> OTHER INFORMATION: synthetic intron where tract of random nucleotides not shown
422 <220> FEATURE:
423 <221> NAME/KEY: misc_feature
424 <222> LOCATION: (1)..(9)
425 <223> OTHER INFORMATION: 5' splice site, where actual splice between nucleotide 3 and
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427 <220> FEATURE:

432 <220> FEATURE:

428 <221> NAME/KEY: misc_feature 429 <222> LOCATION: (10)..(15)

430 <223> OTHER INFORMATION: optional restriction enzyme site

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 12
Seq#:13; N Pos. 16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35
Seq#:13; N Pos. 36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55
Seq#:13; N Pos. 56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75
Seq#:13; N Pos. 76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92
Seq#:16; N Pos. 2
Seq#:18; N Pos. 17
Seq#:19; N Pos. 17

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,13,14,15,16,17,18,19

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/754,014A

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Input Set : A:\09-754,014.txt

L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

Output Set: N:\CRF4\08232004\I754014A.raw

L:529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0

M:341 Repeated in SeqNo=13

L:546 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14

L:551 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14

L:556 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14

L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0

L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0

L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0